IN THE SPECIFICATION:

Please amend paragraph **[0020]** as follows:

[0020] FIG. 1: Junction sequences of T-DNA and *S. cerevisiae* genomic DNA. *S. cerevisiae* YPH250 (WT), *rad50*, *mre11* and *xrs2* strains were cocultivated with LBA1119(pSDM8000). G418-resistant colonies were obtained. Chromosomal DNA was isolated and subjected to Vectorette PCR to determine the sequence of genomic DNA flanking the T-DNA. The position of T-DNA integration was determined by basic BLAST search of the yeast genome at ~~http:/www.genome-stanford.edu/SGD~~ www.genome-stanford.edu/SGD. The Watson strand of genomic DNA that is fused to the LB or RB is shown in italics. Bold sequences represent sequence homology between the LB and target site. The filler DNA sequence is underlined and depicted in italics. The numbers above the LB sequences represent the number of bp deleted from the LB. Tel. = telomeric, Subtel. = subtelomeric and Int. = intergenic.

Please amend paragraph **[0022]** as follows:

[0022] ~~FIG. 3~~ FIGs. 3A and 3B: Alignment of *LIG4* homologues. Sc = *Saccharomyces cerevisiae*, Hs = *Homo sapiens* and At = *Arabidopsis thaliana*. Perfect identity is depicted as black boxes, homology is depicted as grey boxes and dashes are used to optimize alignment. FIG. 3B is a continuation of the alignment presented in FIG. 3A.

Please amend paragraph **[0030]** as follows:

[0030] Chromosomal DNA was isolated using Qiagen's Genomic Tips G/20 per manufacturer's protocol. 1-2 μg of Genomic DNA was digested with *Eco*RI, *Cla*I, *Pst*I or *Hind*III and run on a 1% TBE-gel. Nonradioactive Southern blotting was performed. The membrane was hybridized with a digoxigenine-labeled *kanMX* probe to determine the size of T-DNA/genomic DNA fragments (*Eco*RI and *Cla*I for RB-containing fragments and *Pst*I and *Hind*III for LB-containing fragments). The *kanMX* probe, a 792 bp internal fragment of the *KanMX* marker, was made by PCR using primers *kan*mxp1 5'-AGACTCACGTTTCGAGGCC-3'

and *kan*mxp2 5′-TCACCGAGGCAGTTCCATAG-3′ and a Nonradioactive DNA Labeling and Detection kit (Boehringer Mannheim). The enzyme showing the smallest band on blot was used for Vectorette PCR in order to amplify the smallest junction sequence of T-DNA and genomic DNA. Vectorette PCR was performed as described ~~(http://genomewww.stanford.edu/group/botlab/protocols/vectorette.html)~~ (genomewww.stanford.edu/group/botlab/protocols/vectorette.html). The Expand™ High Fidelity System (Boehringer Mannheim) was used to amplify fragments larger than 2.5 kb, whereas sTaq DNA polymerase (SphaeroQ) was used for amplification of fragments smaller than 2.5 kb. Primers *kan*mxp3 5′-TCGCAGGTCTGCAGCGAGGAGC-3′ and *kan*mxp4 5′-TCGCCTCGACATCATCTGCCCAG-3′ were used to amplify RB/genomic DNA and LB/genomic DNA junction sequences, respectively.

Please amend paragraph **[0035]** as follows:

[0035] We confirmed by PCR that the T-DNA from pSDM8001 became integrated at the *PDA1* locus by homologous recombination (data not shown). In order to find out whether the T-DNA from pSDM8000 had integrated randomly by IR, yeast target sites for integration were determined from eight G418-resistant YPH250 colonies by Vectorette PCR (for detailed description see materials and methods). Chromosomal DNA was isolated and digested with a restriction enzyme that cuts within the T-DNA. A Vectorette was ligated to the digested DNA and a PCR was performed using a T-DNA-specific primer and a Vectorette-specific primer. The PCR product obtained was cloned into pGEMTEasy and sequenced using a T-DNA-specific primer. The position of the T-DNA insertion was determined by basic BLAST search of the yeast genome ~~(http://www-genome.stanford.edu/SGD)~~ (www-genome.stanford.edu/SGD). We were thus able to map the position of the T-DNA insertions of all eight G418-resistant colonies analyzed. They were present at different positions spread out over the genome. Comparison of the T-DNA sequence and yeast target site sequences did not reveal any obvious homology. These data show that the T-DNA from pSDM8000 had integrated via an IR mechanism as expected.

Please amend paragraph **[0043]** as follows:

[0043] From several cocultivation experiments with the *rad50*, *mre11*, *xrs2*, *lig4* and *sir4* mutants, we obtained a small number of G418-resistant colonies. The T-DNA structure was determined for a number of these lines. To this end, chromosomal DNA was isolated from these G418-resistant colonies and subjected to vectorette PCR to amplify junction sequences of genomic DNA and T-DNA. PCR products were cloned and sequenced. The yeast sequences linked to the T-DNA were used in a BLAST search at ~~http://www-genome.stanford.edu/SGD~~ www-genome.stanford.edu/SGD to determine the T-DNA integration sites.